



ALIGNMENT 1: SEQ ID NO:7

Original Seq7	1	30	31	60	61	90	91	120
Substitute Seq7	GAATTCACGATGGCCAAACAATACAAATTC	GAAATCCTGAACAATATCATCTGAACTCG	GAAATCCTGAACAATATCATCTGAACTCG	CGTTACAAAGACAACAATCTGATCGATCTG	CGTTACAAAGACAACAATCTGATCGATCTG	TCTGGTTACGGTGTCAAAGTTGAAGTATAC	TCTGGTTACGGTGTCAAAGTTGAAGTATAC	TCTGGTTACGGTGTCAAAGTTGAAGTATAC
Amended Seq7	GAATTCACGATGGCCAAACAATACAAATTC	GAAATCCTGAACAATATCATCTGAACTCG	GAAATCCTGAACAATATCATCTGAACTCG	CGTTACAAAGACAACAATCTGATCGATCTG	CGTTACAAAGACAACAATCTGATCGATCTG	TCTGGTTACGGTGTCAAAGTTGAAGTATAC	TCTGGTTACGGTGTCAAAGTTGAAGTATAC	TCTGGTTACGGTGTCAAAGTTGAAGTATAC
Original Fig4	GAATTCACGATGGCCAAACAATACAAATTC	GAAATCCTGAACAATATCATCTGAACTCG	GAAATCCTGAACAATATCATCTGAACTCG	CGTTACAAAGACAACAATCTGATCGATCTG	CGTTACAAAGACAACAATCTGATCGATCTG	TCTGGTTACGGTGTCAAAGTTGAAGTATAC	TCTGGTTACGGTGTCAAAGTTGAAGTATAC	TCTGGTTACGGTGTCAAAGTTGAAGTATAC
Original Seq7	121	150	151	180	181	210	211	240
Substitute Seq7	GACGGTGTGAAGTGAATGACAAGAACCCAG	TTCAAACTGACCTCTTCGCTAACTCTAAG	TTCAAACTGACCTCTTCGCTAACTCTAAG	ATCCGTGTACTCAGAATCAGAACATCATC	ATCCGTGTACTCAGAATCAGAACATCATC	TTCAACTCCGTATTCTCGGACTTCTCTGTT	TTCAACTCCGTATTCTCGGACTTCTCTGTT	TTCAACTCCGTATTCTCGGACTTCTCTGTT
Amended Seq7	GACGGTGTGAAGTGAATGACAAGAACCCAG	TTCAAACTGACCTCTTCGCTAACTCTAAG	TTCAAACTGACCTCTTCGCTAACTCTAAG	ATCCGTGTACTCAGAATCAGAACATCATC	ATCCGTGTACTCAGAATCAGAACATCATC	TTCAACTCCGTATTCTCGGACTTCTCTGTT	TTCAACTCCGTATTCTCGGACTTCTCTGTT	TTCAACTCCGTATTCTCGGACTTCTCTGTT
Original Fig4	GACGGTGTGAAGTGAATGACAAGAACCCAG	TTCAAACTGACCTCTTCGCTAACTCTAAG	TTCAAACTGACCTCTTCGCTAACTCTAAG	ATCCGTGTACTCAGAATCAGAACATCATC	ATCCGTGTACTCAGAATCAGAACATCATC	TTCAACTCCGTATTCTCGGACTTCTCTGTT	TTCAACTCCGTATTCTCGGACTTCTCTGTT	TTCAACTCCGTATTCTCGGACTTCTCTGTT
Original Seq7	241	270	271	300	301	330	331	360
Substitute Seq7	TCCTTCTGGATTCGTATCCCGAAATACAAG	AACGACGGTATCCAGAATTACATCCACAAT	AACGACGGTATCCAGAATTACATCCACAAT	GAATACACCATCATCAACTGCATGAAGAAT	GAATACACCATCATCAACTGCATGAAGAAT	AACCTCTGGTTGGAAGATCTCCATCCCGGT	AACCTCTGGTTGGAAGATCTCCATCCCGGT	AACCTCTGGTTGGAAGATCTCCATCCCGGT
Amended Seq7	TCCTTCTGGATTCGTATCCCGAAATACAAG	AACGACGGTATCCAGAATTACATCCACAAT	AACGACGGTATCCAGAATTACATCCACAAT	GAATACACCATCATCAACTGCATGAAGAAT	GAATACACCATCATCAACTGCATGAAGAAT	AACCTCTGGTTGGAAGATCTCCATCCCGGT	AACCTCTGGTTGGAAGATCTCCATCCCGGT	AACCTCTGGTTGGAAGATCTCCATCCCGGT
Original Fig4	TCCTTCTGGATTCGTATCCCGAAATACAAG	AACGACGGTATCCAGAATTACATCCACAAT	AACGACGGTATCCAGAATTACATCCACAAT	GAATACACCATCATCAACTGCATGAAGAAT	GAATACACCATCATCAACTGCATGAAGAAT	AACCTCTGGTTGGAAGATCTCCATCCCGGT	AACCTCTGGTTGGAAGATCTCCATCCCGGT	AACCTCTGGTTGGAAGATCTCCATCCCGGT
Original Seq7	361	390	391	420	421	450	451	480
Substitute Seq7	AACGGTATCATCTGGACTCTGATCGATATC	AACGGTAAAGACCAAAATCTGTATTCTTCGAA	AACGGTAAAGACCAAAATCTGTATTCTTCGAA	TACAACATCCGTGAAGACATCTCTGAATAC	TACAACATCCGTGAAGACATCTCTGAATAC	ATCAATCCGTGGTTCTTCGTTACCATCACC	ATCAATCCGTGGTTCTTCGTTACCATCACC	ATCAATCCGTGGTTCTTCGTTACCATCACC
Amended Seq7	AACGGTATCATCTGGACTCTGATCGATATC	AACGGTAAAGACCAAAATCTGTATTCTTCGAA	AACGGTAAAGACCAAAATCTGTATTCTTCGAA	TACAACATCCGTGAAGACATCTCTGAATAC	TACAACATCCGTGAAGACATCTCTGAATAC	ATCAATCCGTGGTTCTTCGTTACCATCACC	ATCAATCCGTGGTTCTTCGTTACCATCACC	ATCAATCCGTGGTTCTTCGTTACCATCACC
Original Fig4	AACGGTATCATCTGGACTCTGATCGATATC	AACGGTAAAGACCAAAATCTGTATTCTTCGAA	AACGGTAAAGACCAAAATCTGTATTCTTCGAA	TACAACATCCGTGAAGACATCTCTGAATAC	TACAACATCCGTGAAGACATCTCTGAATAC	ATCAATCCGTGGTTCTTCGTTACCATCACC	ATCAATCCGTGGTTCTTCGTTACCATCACC	ATCAATCCGTGGTTCTTCGTTACCATCACC
Original Seq7	481	510	511	540	541	570	571	600
Substitute Seq7	AATAACCTGAACAATGCTAAAATCTACATC	AACGGTAAACTGGAATCTAATACCGACATC	AACGGTAAACTGGAATCTAATACCGACATC	AAAGACATCCGTGAAGTTATCGCTAACGGT	AAAGACATCCGTGAAGTTATCGCTAACGGT	GAAATCATCTTCAAACCTGGACGGTGACATC	GAAATCATCTTCAAACCTGGACGGTGACATC	GAAATCATCTTCAAACCTGGACGGTGACATC
Amended Seq7	AATAACCTGAACAATGCTAAAATCTACATC	AACGGTAAACTGGAATCTAATACCGACATC	AACGGTAAACTGGAATCTAATACCGACATC	AAAGACATCCGTGAAGTTATCGCTAACGGT	AAAGACATCCGTGAAGTTATCGCTAACGGT	GAAATCATCTTCAAACCTGGACGGTGACATC	GAAATCATCTTCAAACCTGGACGGTGACATC	GAAATCATCTTCAAACCTGGACGGTGACATC
Original Fig4	AATAACCTGAACAATGCTAAAATCTACATC	AACGGTAAACTGGAATCTAATACCGACATC	AACGGTAAACTGGAATCTAATACCGACATC	AAAGACATCCGTGAAGTTATCGCTAACGGT	AAAGACATCCGTGAAGTTATCGCTAACGGT	GAAATCATCTTCAAACCTGGACGGTGACATC	GAAATCATCTTCAAACCTGGACGGTGACATC	GAAATCATCTTCAAACCTGGACGGTGACATC
Original Seq7	601	630	631	660	661	690	691	720
Substitute Seq7	GATCGTACCCAGTTTCATCTGGATGAAATAC	TTCCTCATCTTCAACACCGAACTGTCTCAG	TTCCTCATCTTCAACACCGAACTGTCTCAG	TCCAATATCGAAGAACCGTACAAGATCCAG	TCCAATATCGAAGAACCGTACAAGATCCAG	TCTTACTCCGAATACCTGAAAGACTTCTGG	TCTTACTCCGAATACCTGAAAGACTTCTGG	TCTTACTCCGAATACCTGAAAGACTTCTGG
Amended Seq7	GATCGTACCCAGTTTCATCTGGATGAAATAC	TTCCTCATCTTCAACACCGAACTGTCTCAG	TTCCTCATCTTCAACACCGAACTGTCTCAG	TCCAATATCGAAGAACCGTACAAGATCCAG	TCCAATATCGAAGAACCGTACAAGATCCAG	TCTTACTCCGAATACCTGAAAGACTTCTGG	TCTTACTCCGAATACCTGAAAGACTTCTGG	TCTTACTCCGAATACCTGAAAGACTTCTGG
Original Fig4	GATCGTACCCAGTTTCATCTGGATGAAATAC	TTCCTCATCTTCAACACCGAACTGTCTCAG	TTCCTCATCTTCAACACCGAACTGTCTCAG	TCCAATATCGAAGAACCGTACAAGATCCAG	TCCAATATCGAAGAACCGTACAAGATCCAG	TCTTACTCCGAATACCTGAAAGACTTCTGG	TCTTACTCCGAATACCTGAAAGACTTCTGG	TCTTACTCCGAATACCTGAAAGACTTCTGG
Original Seq7	721	750	751	780	781	810	811	840
Substitute Seq7	GGTAATCCGCTGATGTACAACAAGAAATAC	TATATGTTCAATGCTGGTAAACAAGAACTCT	TATATGTTCAATGCTGGTAAACAAGAACTCT	TACATCAAACCTGAAGAAAGACTCTCCGGTT	TACATCAAACCTGAAGAAAGACTCTCCGGTT	GGTGAAATCCCTGACTCGTTCCAAATACAAC	GGTGAAATCCCTGACTCGTTCCAAATACAAC	GGTGAAATCCCTGACTCGTTCCAAATACAAC
Amended Seq7	GGTAATCCGCTGATGTACAACAAGAAATAC	TATATGTTCAATGCTGGTAAACAAGAACTCT	TATATGTTCAATGCTGGTAAACAAGAACTCT	TACATCAAACCTGAAGAAAGACTCTCCGGTT	TACATCAAACCTGAAGAAAGACTCTCCGGTT	GGTGAAATCCCTGACTCGTTCCAAATACAAC	GGTGAAATCCCTGACTCGTTCCAAATACAAC	GGTGAAATCCCTGACTCGTTCCAAATACAAC
Original Fig4	GGTAATCCGCTGATGTACAACAAGAAATAC	TATATGTTCAATGCTGGTAAACAAGAACTCT	TATATGTTCAATGCTGGTAAACAAGAACTCT	TACATCAAACCTGAAGAAAGACTCTCCGGTT	TACATCAAACCTGAAGAAAGACTCTCCGGTT	GGTGAAATCCCTGACTCGTTCCAAATACAAC	GGTGAAATCCCTGACTCGTTCCAAATACAAC	GGTGAAATCCCTGACTCGTTCCAAATACAAC
Original Seq7	841	870	871	900	901	930	931	960
Substitute Seq7	CAGAACTCTAAATACATCAACTACCGCGAC	CTGTACATCGGTGAAAAGTTTCATCATCCGT	CTGTACATCGGTGAAAAGTTTCATCATCCGT	CGCAAACTCTAACTCTCAGTCCATCAATGAT	CGCAAACTCTAACTCTCAGTCCATCAATGAT	GACATCGTACGTAAGAAGACTACATCTAC	GACATCGTACGTAAGAAGACTACATCTAC	GACATCGTACGTAAGAAGACTACATCTAC
Amended Seq7	CAGAACTCTAAATACATCAACTACCGCGAC	CTGTACATCGGTGAAAAGTTTCATCATCCGT	CTGTACATCGGTGAAAAGTTTCATCATCCGT	CGCAAACTCTAACTCTCAGTCCATCAATGAT	CGCAAACTCTAACTCTCAGTCCATCAATGAT	GACATCGTACGTAAGAAGACTACATCTAC	GACATCGTACGTAAGAAGACTACATCTAC	GACATCGTACGTAAGAAGACTACATCTAC
Original Fig4	CAGAACTCTAAATACATCAACTACCGCGAC	CTGTACATCGGTGAAAAGTTTCATCATCCGT	CTGTACATCGGTGAAAAGTTTCATCATCCGT	CGCAAACTCTAACTCTCAGTCCATCAATGAT	CGCAAACTCTAACTCTCAGTCCATCAATGAT	GACATCGTACGTAAGAAGACTACATCTAC	GACATCGTACGTAAGAAGACTACATCTAC	GACATCGTACGTAAGAAGACTACATCTAC
Original Seq7	961	990	991	1020	1021	1050	1051	1080
Substitute Seq7	CTGGACTTCTTCAACCTGAATCAGGAATGG	CGTGATACACCTACAAGTACTTCAAGAAA	CGTGATACACCTACAAGTACTTCAAGAAA	GAAGAAGAAAAGCTTTTCCTGGCTCCGATC	GAAGAAGAAAAGCTTTTCCTGGCTCCGATC	TCTGATTCCGACGAACCTCTACAACACCATC	TCTGATTCCGACGAACCTCTACAACACCATC	TCTGATTCCGACGAACCTCTACAACACCATC
Amended Seq7	CTGGACTTCTTCAACCTGAATCAGGAATGG	CGTGATACACCTACAAGTACTTCAAGAAA	CGTGATACACCTACAAGTACTTCAAGAAA	GAAGAAGAAAAGCTTTTCCTGGCTCCGATC	GAAGAAGAAAAGCTTTTCCTGGCTCCGATC	TCTGATTCCGACGAACCTCTACAACACCATC	TCTGATTCCGACGAACCTCTACAACACCATC	TCTGATTCCGACGAACCTCTACAACACCATC
Original Fig4	CTGGACTTCTTCAACCTGAATCAGGAATGG	CGTGATACACCTACAAGTACTTCAAGAAA	CGTGATACACCTACAAGTACTTCAAGAAA	GAAGAAGAAAAGCTTTTCCTGGCTCCGATC	GAAGAAGAAAAGCTTTTCCTGGCTCCGATC	TCTGATTCCGACGAACCTCTACAACACCATC	TCTGATTCCGACGAACCTCTACAACACCATC	TCTGATTCCGACGAACCTCTACAACACCATC
Original Seq7	1081	1110	1111	1140	1141	1170	1171	1200
Substitute Seq7	CAGATCAAAGAATACGACGAACAGCCGACC	TACTCTTGCCAGCTGCTGTTCAAGAAAGAT	TACTCTTGCCAGCTGCTGTTCAAGAAAGAT	GAAGAATCTACTGACGAAATCGGTCTGATC	GAAGAATCTACTGACGAAATCGGTCTGATC	GGTATCCACCGTTTCTACGAATCTGGTATC	GGTATCCACCGTTTCTACGAATCTGGTATC	GGTATCCACCGTTTCTACGAATCTGGTATC
Amended Seq7	CAGATCAAAGAATACGACGAACAGCCGACC	TACTCTTGCCAGCTGCTGTTCAAGAAAGAT	TACTCTTGCCAGCTGCTGTTCAAGAAAGAT	GAAGAATCTACTGACGAAATCGGTCTGATC	GAAGAATCTACTGACGAAATCGGTCTGATC	GGTATCCACCGTTTCTACGAATCTGGTATC	GGTATCCACCGTTTCTACGAATCTGGTATC	GGTATCCACCGTTTCTACGAATCTGGTATC
Original Fig4	CAGATCAAAGAATACGACGAACAGCCGACC	TACTCTTGCCAGCTGCTGTTCAAGAAAGAT	TACTCTTGCCAGCTGCTGTTCAAGAAAGAT	GAAGAATCTACTGACGAAATCGGTCTGATC	GAAGAATCTACTGACGAAATCGGTCTGATC	GGTATCCACCGTTTCTACGAATCTGGTATC	GGTATCCACCGTTTCTACGAATCTGGTATC	GGTATCCACCGTTTCTACGAATCTGGTATC
Original Seq7	1201	1230	1231	1260	1261	1290	1291	1320
Substitute Seq7	GTATTGGAAGAATACAAAGACTACTTCTGC	ATCTCCAAATGGTACCTGAAGGAAGTTAAA	ATCTCCAAATGGTACCTGAAGGAAGTTAAA	CGCAAAACCGTACAACCTGAAACTGGGTTCG	CGCAAAACCGTACAACCTGAAACTGGGTTCG	AATTGGCAGTTTCATCCCGAAGACGAAGGT	AATTGGCAGTTTCATCCCGAAGACGAAGGT	AATTGGCAGTTTCATCCCGAAGACGAAGGT
Amended Seq7	GTATTGGAAGAATACAAAGACTACTTCTGC	ATCTCCAAATGGTACCTGAAGGAAGTTAAA	ATCTCCAAATGGTACCTGAAGGAAGTTAAA	CGCAAAACCGTACAACCTGAAACTGGGTTCG	CGCAAAACCGTACAACCTGAAACTGGGTTCG	AATTGGCAGTTTCATCCCGAAGACGAAGGT	AATTGGCAGTTTCATCCCGAAGACGAAGGT	AATTGGCAGTTTCATCCCGAAGACGAAGGT
Original Fig4	GTATTGGAAGAATACAAAGACTACTTCTGC	ATCTCCAAATGGTACCTGAAGGAAGTTAAA	ATCTCCAAATGGTACCTGAAGGAAGTTAAA	CGCAAAACCGTACAACCTGAAACTGGGTTCG	CGCAAAACCGTACAACCTGAAACTGGGTTCG	AATTGGCAGTTTCATCCCGAAGACGAAGGT	AATTGGCAGTTTCATCCCGAAGACGAAGGT	AATTGGCAGTTTCATCCCGAAGACGAAGGT
Original Seq7	1321	1341						
Substitute Seq7	TGGACCGAATAGTAAGAATTC	TGGACCGAATAGTAAGAATTC						
Amended Seq7	TGGACCGAATAGTAAGAATTC	TGGACCGAATAGTAAGAATTC						
Original Fig4	TGGACCGAATAGTAAGAATTC	TGGACCGAATAGTAAGAATTC						

ALIGNMENT 2: SEQ ID NO:37

Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1 CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT CTCGAGCCATGGCTCGTCTGCTGTCTACCT *****	30 TCCTGAATACATCAAGAATCATCAATA TCCTGAATACATCAAGAATCATCAATA TCCTGAATACATCAAGAATCATCAATA TCCTGAATACATCAAGAATCATCAATA *****	60 CCTCCATCTGAACTGCGCTACGAATCCA CCTCCATCTGAACTGCGCTACGAATCCA CCTCCATCTGAACTGCGCTACGAATCCA CCTCCATCTGAACTGCGCTACGAATCCA *****	90 ATCACCTGATCGACCTGTCTCGGTACGCTT ATCACCTGATCGACCTGTCTCGGTACGCTT ATCACCTGATCGACCTGTCTCGGTACGCTT ATCACCTGATCGACCTGTCTCGGTACGCTT *****	120 TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	121 CCAAAAATCAACATCGGTTCTAAATTTAACT CCAAAAATCAACATCGGTTCTAAATTTAACT CCAAAAATCAACATCGGTTCTAAATTTAACT CCAAAAATCAACATCGGTTCTAAATTTAACT *****	150 TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATCGACAAGAATCAGATCCAGC TCGATCCGATCGACAAGAATCAGATCCAGC *****	180 TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG TGTTCAATCTGGAATCTTCCAAAATCGAAG *****	210 TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT *****	240 TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT TTATCTCTGAAGAATGCTATCGTATACAAT *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	241 CTATGTACGAAAACCTTCTCCACCTCCTTCT CTATGTACGAAAACCTTCTCCACCTCCTTCT CTATGTACGAAAACCTTCTCCACCTCCTTCT CTATGTACGAAAACCTTCTCCACCTCCTTCT *****	270 GGATCCGATCCGAAAATCTTCAACTCCA GGATCCGATCCGAAAATCTTCAACTCCA GGATCCGATCCGAAAATCTTCAACTCCA GGATCCGATCCGAAAATCTTCAACTCCA *****	300 TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA TCTCTCTGAACAATGAATACACCATCATCA *****	330 ACTGTCATGAAAAACAATCTCGTGTGGAAAG ACTGTCATGAAAAACAATCTCGTGTGGAAAG ACTGTCATGAAAAACAATCTCGTGTGGAAAG ACTGTCATGAAAAACAATCTCGTGTGGAAAG *****	360 ACTGTCATGAAAAACAATCTCGTGTGGAAAG ACTGTCATGAAAAACAATCTCGTGTGGAAAG ACTGTCATGAAAAACAATCTCGTGTGGAAAG ACTGTCATGAAAAACAATCTCGTGTGGAAAG *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	361 TATCTCTGAACACGTTGAAATCATCTGGA TATCTCTGAACACGTTGAAATCATCTGGA TATCTCTGAACACGTTGAAATCATCTGGA TATCTCTGAACACGTTGAAATCATCTGGA *****	390 CTCTGCAGGACACTCAGGAATCAACACAGC CTCTGCAGGACACTCAGGAATCAACACAGC CTCTGCAGGACACTCAGGAATCAACACAGC CTCTGCAGGACACTCAGGAATCAACACAGC *****	420 GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA GTGTTGTATTCAAATACTCTCAGATGATCA *****	450 ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT *****	480 ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT ACATCTCTGACTACATCAATCGCTGGATCT *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	481 TCGTTACCACACCAACATCGTCTGAATA TCGTTACCACACCAACATCGTCTGAATA TCGTTACCACACCAACATCGTCTGAATA TCGTTACCACACCAACATCGTCTGAATA *****	510 ACTCCAAAATCTACATCAACGTCGGTCTGA ACTCCAAAATCTACATCAACGTCGGTCTGA ACTCCAAAATCTACATCAACGTCGGTCTGA ACTCCAAAATCTACATCAACGTCGGTCTGA *****	540 TCGACAGAAACCGATCTCCAATCTGGGTA TCGACAGAAACCGATCTCCAATCTGGGTA TCGACAGAAACCGATCTCCAATCTGGGTA TCGACAGAAACCGATCTCCAATCTGGGTA *****	570 ACATCCACGTTCTTAATAACATCATGTTTCA ACATCCACGTTCTTAATAACATCATGTTTCA ACATCCACGTTCTTAATAACATCATGTTTCA ACATCCACGTTCTTAATAACATCATGTTTCA *****	600 ACATCCACGTTCTTAATAACATCATGTTTCA ACATCCACGTTCTTAATAACATCATGTTTCA ACATCCACGTTCTTAATAACATCATGTTTCA ACATCCACGTTCTTAATAACATCATGTTTCA *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	601 AATCGGACGGTTGTCGTGACACTCACCCT AATCGGACGGTTGTCGTGACACTCACCCT AATCGGACGGTTGTCGTGACACTCACCCT AATCGGACGGTTGTCGTGACACTCACCCT *****	630 ACATCTGGATCAAAATCTTCAATCTGTTTCG ACATCTGGATCAAAATCTTCAATCTGTTTCG ACATCTGGATCAAAATCTTCAATCTGTTTCG ACATCTGGATCAAAATCTTCAATCTGTTTCG *****	660 ACAAAGAACTGAACGAAAAAGAAATCAAG ACAAAGAACTGAACGAAAAAGAAATCAAG ACAAAGAACTGAACGAAAAAGAAATCAAG ACAAAGAACTGAACGAAAAAGAAATCAAG *****	690 ACCTGTACGACAACCAAGTCCAATCTCGGTA ACCTGTACGACAACCAAGTCCAATCTCGGTA ACCTGTACGACAACCAAGTCCAATCTCGGTA ACCTGTACGACAACCAAGTCCAATCTCGGTA *****	720 ACCTGTACGACAACCAAGTCCAATCTCGGTA ACCTGTACGACAACCAAGTCCAATCTCGGTA ACCTGTACGACAACCAAGTCCAATCTCGGTA ACCTGTACGACAACCAAGTCCAATCTCGGTA *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	721 TCCCTGAAAGACTTCTGGGGTGACTACCTGC TCCCTGAAAGACTTCTGGGGTGACTACCTGC TCCCTGAAAGACTTCTGGGGTGACTACCTGC TCCCTGAAAGACTTCTGGGGTGACTACCTGC *****	750 AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC AGTACGACAAACCGTACTACATGCTGAATC *****	780 TGTCACGATCCGAAACAAATACGTTGACGTC TGTCACGATCCGAAACAAATACGTTGACGTC TGTCACGATCCGAAACAAATACGTTGACGTC TGTCACGATCCGAAACAAATACGTTGACGTC *****	810 ACAATGTAGGTATCCCGGGTTACATGTATCC ACAATGTAGGTATCCCGGGTTACATGTATCC ACAATGTAGGTATCCCGGGTTACATGTATCC ACAATGTAGGTATCCCGGGTTACATGTATCC *****	840 ACAATGTAGGTATCCCGGGTTACATGTATCC ACAATGTAGGTATCCCGGGTTACATGTATCC ACAATGTAGGTATCCCGGGTTACATGTATCC ACAATGTAGGTATCCCGGGTTACATGTATCC *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	841 TGAAAGGTCGCGGTGGTCTGTTATGACTA TGAAAGGTCGCGGTGGTCTGTTATGACTA TGAAAGGTCGCGGTGGTCTGTTATGACTA TGAAAGGTCGCGGTGGTCTGTTATGACTA *****	870 CCAACATCTACCTGAACCTTCCCTGTGACC CCAACATCTACCTGAACCTTCCCTGTGACC CCAACATCTACCTGAACCTTCCCTGTGACC CCAACATCTACCTGAACCTTCCCTGTGACC *****	900 GTGGTACCAAAATTCATCATCAAGAAATACG GTGGTACCAAAATTCATCATCAAGAAATACG GTGGTACCAAAATTCATCATCAAGAAATACG GTGGTACCAAAATTCATCATCAAGAAATACG *****	930 CGTCTGGTAAACAGGACAATATCGTTCGCA CGTCTGGTAAACAGGACAATATCGTTCGCA CGTCTGGTAAACAGGACAATATCGTTCGCA CGTCTGGTAAACAGGACAATATCGTTCGCA *****	960 CGTCTGGTAAACAGGACAATATCGTTCGCA CGTCTGGTAAACAGGACAATATCGTTCGCA CGTCTGGTAAACAGGACAATATCGTTCGCA CGTCTGGTAAACAGGACAATATCGTTCGCA *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	961 ACAATGATCGGTATACATCAATGTTGTAG ACAATGATCGGTATACATCAATGTTGTAG ACAATGATCGGTATACATCAATGTTGTAG ACAATGATCGGTATACATCAATGTTGTAG *****	990 TTAAGAACAAAGAAATACCGTCTGGCTACCA TTAAGAACAAAGAAATACCGTCTGGCTACCA TTAAGAACAAAGAAATACCGTCTGGCTACCA TTAAGAACAAAGAAATACCGTCTGGCTACCA *****	1020 ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT ATGCTTCTCAGGCTGGTGTAGAAAAGATCT *****	1050 TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA *****	1080 TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA TGCTCTGCTCTGGAATCCCGGACGTTGGTA *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1081 ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA ATCTGTCTCAGGTAGTTGTAATGAAATCCA *****	1110 AGAACGACCAAGGATCACTAACAAATGCA AGAACGACCAAGGATCACTAACAAATGCA AGAACGACCAAGGATCACTAACAAATGCA AGAACGACCAAGGATCACTAACAAATGCA *****	1140 AAATGAATCTGCAGGACAACAAATGTAACG AAATGAATCTGCAGGACAACAAATGTAACG AAATGAATCTGCAGGACAACAAATGTAACG AAATGAATCTGCAGGACAACAAATGTAACG *****	1170 ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA *****	1200 ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA ATATCGGTTTTCATCGGTTTCCACCAAGTTCA *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1201 ACAATATCGCTAACTGGTGTCTTCCAAC ACAATATCGCTAACTGGTGTCTTCCAAC ACAATATCGCTAACTGGTGTCTTCCAAC ACAATATCGCTAACTGGTGTCTTCCAAC *****	1230 GGTACAATCGTCAGATCGAAGTTCCTCTC GGTACAATCGTCAGATCGAAGTTCCTCTC GGTACAATCGTCAGATCGAAGTTCCTCTC GGTACAATCGTCAGATCGAAGTTCCTCTC *****	1260 GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC GCACCTCTGGGTTGCTCTTGGGAGTTTCATCC *****	1290 CGGTTGATGACGGTTGGGGTGAACGTCGCC CGGTTGATGACGGTTGGGGTGAACGTCGCC CGGTTGATGACGGTTGGGGTGAACGTCGCC CGGTTGATGACGGTTGGGGTGAACGTCGCC *****	1320 CGGTTGATGACGGTTGGGGTGAACGTCGCC CGGTTGATGACGGTTGGGGTGAACGTCGCC CGGTTGATGACGGTTGGGGTGAACGTCGCC CGGTTGATGACGGTTGGGGTGAACGTCGCC *****
Original_Seq37 Substitute_Seq37 Amended_Seq37 Fig2_ '975_App	1321 TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT *****	1338 TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT TGTAACCCGGGAAAGCTT *****			

ALIGNMENT 3: SEQ ID NO:39

Original_Seq39	1	30	31	60	61	90	91	120
Substitute_Seq39	ATGGC	CAACAAATACAATTCGAAATC	CTGAAACAATATCATCTGGAACCTGCGTTAC	AAAGACAACAATCTGATCGATCTGTCTGGT	TACGGTGTCAAAGTTGAAGTATACGACGGT			
Amended_Seq39	ATGGC	CAACAAATACAATTCGAAATC	CTGAAACAATATCATCTGGAACCTGCGTTAC	AAAGACAACAATCTGATCGATCTGTCTGGT	TACGGTGTCAAAGTTGAAGTATACGACGGT			
Fig4_ '975_App	ATGGC	CAACAAATACAATTCGAAATC	CTGAAACAATATCATCTGGAACCTGCGTTAC	AAAGACAACAATCTGATCGATCTGTCTGGT	TACGGTGTCAAAGTTGAAGTATACGACGGT			
Original_Seq39	121	150	151	180	181	210	211	240
Substitute_Seq39	GTTGAACTGAATGACAAGAACCAGTTCAAA	CTGACCTCTTCGCTAACTCTAAGATCCGT	GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC				
Amended_Seq39	GTTGAACTGAATGACAAGAACCAGTTCAAA	CTGACCTCTTCGCTAACTCTAAGATCCGT	GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC				
Fig4_ '975_App	GTTGAACTGAATGACAAGAACCAGTTCAAA	CTGACCTCTTCGCTAACTCTAAGATCCGT	GTTACTCAGAATCAGAACATCATCTTCAAC	TCCGTATTCCTGGACTTCTCTGTTTCCTTC				
Original_Seq39	241	270	271	300	301	330	331	360
Substitute_Seq39	TGGATCCGTATCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCCAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCCGGTAACCGT				
Amended_Seq39	TGGATCCGTATCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCCAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCCGGTAACCGT				
Fig4_ '975_App	TGGATCCGTATCCGAAATACAAGAACGAC	GGTATCCAGAATTACATCCCAATGAATAC	ACCATCATCAACTGCATGAAGAATAACTCT	GGTTGGAAGATCTCCATCCCGGTAACCGT				
Original_Seq39	361	390	391	420	421	450	451	480
Substitute_Seq39	ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAATCTGTATTCTTCAATACAAC	ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTCTTCGTTACCACCAATAAAC				
Amended_Seq39	ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAATCTGTATTCTTCAATACAAC	ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTCTTCGTTACCACCAATAAAC				
Fig4_ '975_App	ATCATCTGGACTCTGATCGATATCAACGGT	AAGACCAATCTGTATTCTTCAATACAAC	ATCCGTGAAGACATCTCTGAATACATCAAT	CGCTGGTCTTCGTTACCACCAATAAAC				
Original_Seq39	481	510	511	540	541	570	571	600
Substitute_Seq39	CTGAACAATGCTAAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAGAC	ATCCGTGAAGTATTCGCTAACGGTGAATTC	ATCTTCAAACCTGGACGGTGACATCGATCGT				
Amended_Seq39	CTGAACAATGCTAAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAGAC	ATCCGTGAAGTATTCGCTAACGGTGAATTC	ATCTTCAAACCTGGACGGTGACATCGATCGT				
Fig4_ '975_App	CTGAACAATGCTAAAATCTACATCAACGGT	AAACTGGAATCTAATACCGACATCAAGAC	ATCCGTGAAGTATTCGCTAACGGTGAATTC	ATCTTCAAACCTGGACGGTGACATCGATCGT				
Original_Seq39	601	630	631	660	661	690	691	720
Substitute_Seq39	ACCCAGTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAATGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT				
Amended_Seq39	ACCCAGTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAATGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT				
Fig4_ '975_App	ACCCAGTTCATCTGGATGAAATACTTCTCC	ATCTTCAACACCGAATGTCTCAGTCCAAT	ATCGAAGAACGGTACAAGATCCAGTCTTAC	TCCGAATACCTGAAAGACTTCTGGGGTAAT				
Original_Seq39	721	750	751	780	781	810	811	840
Substitute_Seq39	CCGCTGATGTACAACAAGAATACTATATG	TTCAATGCTGGTAAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA	ATCTTCAACCTGGTCCAAATACAACAGAAC				
Amended_Seq39	CCGCTGATGTACAACAAGAATACTATATG	TTCAATGCTGGTAAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA	ATCTTCAACCTGGTCCAAATACAACAGAAC				
Fig4_ '975_App	CCGCTGATGTACAACAAGAATACTATATG	TTCAATGCTGGTAAACAAGAACTCTTACATC	AAACTGAAGAAAGACTCTCCGGTTGGTGAA	ATCTTCAACCTGGTCCAAATACAACAGAAC				
Original_Seq39	841	870	871	900	901	930	931	960
Substitute_Seq39	TCTAAATACATCAACTACCGGACCTGTAC	ATCGGTGAAAAGTTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGAGACATC	GTACGTAAAGAAGACTACATCTACCTGGAC				
Amended_Seq39	TCTAAATACATCAACTACCGGACCTGTAC	ATCGGTGAAAAGTTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGAGACATC	GTACGTAAAGAAGACTACATCTACCTGGAC				
Fig4_ '975_App	TCTAAATACATCAACTACCGGACCTGTAC	ATCGGTGAAAAGTTTCATCATCCGTCGCAAA	TCTAACTCTCAGTCCATCAATGAGACATC	GTACGTAAAGAAGACTACATCTACCTGGAC				
Original_Seq39	961	990	991	1020	1021	1050	1051	1080
Substitute_Seq39	TTCTTCAACCTGAATCAAGAAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAGAA	GAAAAGCTTTTCTCGGCTCCGATCTCTGAT	TCCGACGAACCTCTACAACACCATCCAGATC				
Amended_Seq39	TTCTTCAACCTGAATCAAGAAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAGAA	GAAAAGCTTTTCTCGGCTCCGATCTCTGAT	TCCGACGAACCTCTACAACACCATCCAGATC				
Fig4_ '975_App	TTCTTCAACCTGAATCAAGAAATGGCGTGTA	TACACCTACAAGTACTTCAAGAAAGAGAA	GAAAAGCTTTTCTCGGCTCCGATCTCTGAT	TCCGACGAACCTCTACAACACCATCCAGATC				
Original_Seq39	1081	1110	1111	1140	1141	1170	1171	1200
Substitute_Seq39	AAAGAATACGACGAACAGCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC				
Amended_Seq39	AAAGAATACGACGAACAGCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC				
Fig4_ '975_App	AAAGAATACGACGAACAGCGACCTACTCT	TGCCAGCTGCTGTTCAAGAAAGATGAAGAA	TCTACTGACGAAATCGGTCTGATCGGTATC	CACCGTTTCTACGAATCTGGTATCGTATTC				
Original_Seq39	1201	1230	1231	1260	1261	1290	1291	1320
Substitute_Seq39	GAAGAATACAAAGACTCTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTCATCCCGAAAGACGAAGGTTGGACC				
Amended_Seq39	GAAGAATACAAAGACTCTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTCATCCCGAAAGACGAAGGTTGGACC				
Fig4_ '975_App	GAAGAATACAAAGACTCTTCTGCATCTCC	AAATGGTACCTGAAGGAAGTTAAACGCAAA	CCGTACAACCTGAAACTGGGTTGCAATTGG	CAGTTCATCCCGAAAGACGAAGGTTGGACC				
Original_Seq39	1321	1350	1351					
Substitute_Seq39	GAATAGTAACCTCTAGAGTCGAGGCCTGCA	G						
Amended_Seq39	GAATAGTAACCTCTAGAGTCGAGGCCTGCA	G						
Fig4_ '975_App	GAATAGTAACCTCTAGAGTCGAGGCCTGCA	G						

ALIGNMENT 4: SEQ ID NO:40

Original_Seq40	1	30 31	60 61	90 91	120
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	MPVTINNFNYPNDPIDNNNIIMMEPPFARGT	GRYYKAFKITDRIWIIIPERYTPGYKPEDFN	KSSGIFNRDVCYYDDPYLNTNDKKNIFLO	TMIKLFNRIKSKPLGKLEMIINGIPYLG	
Original_Seq40	121	150 151	180 181	210 211	240
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	DRRVPLEEFNTNIASVTNKLISNPGEVER	KKGIFANLIIFGPGPVLNENETIDIGIQNH	PASREGFGGIMQMKFCPEYVSVFNNVQENK	GASIFNRRGYFSDPALILMHILHVLHGLY	
Original_Seq40	241	270 271	300 301	330 331	360
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	GIKVDDLPIVNEKKFFMQSTDAIQAEELY	TFGGQDPSIITPSTDKSIYDKVLQNFGRIV	DRLNKVLVCISDPNININIIYKNKFKDKYKF	VEDSEGKYSIDVESFDKLYKSLMFGFTETN	
Original_Seq40	361	390 391	420 421	450 451	480
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	IAENYKIKTRASYSFSDSLPPVKIKNLLDNE	IYTIIEGFPNISDKMEKEYRGQNKAIKQA	YEEISKEHLAVYKIQMCKSVKAPGICIDVD	NEDLFFIADKNSFSDLSKNERIEYNTQSN	
Original_Seq40	481	510 511	540 541	570 571	600
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	YIENDFPINELILDTLISKIELPSENTES	LTDNFVDVPVYEKQPAIKKIPTDENTIFQY	LYSQTPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLPAGVWQIVND	
Original_Seq40	601	630 631	660 661	690 691	720
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	FVIEANKSNTMDKRIADISLIPVYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTQRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	
Original_Seq40	721	750 751	780 781	810 811	840
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	KALNYQAQALEBIIKYRYNIYSEKEKSNIN	IDFNDINSKLNIGINQAIDNINNFIGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLLNYI	DENKLYLIGSAEYKSKVNKYLKTIIMPFDL	
Original_Seq40	841	870 871	900 901	930 931	960
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	-----FNKYNSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	-----FNKYNSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	-----FNKYNSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	SIYTNDTILIEMFNKNYSEILNIIILNLRY	KDNNLIDLSGYGAKVEYDGVLENDKNQFK	LTSSANSKIRVTQNQNIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCCKNNS	
	*****	*****	*****	*****	
Original_Seq40	961	990 991	1020 1021	1050 1051	1080
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	GWKISIRGNRIWTLIDINGTKTSVFFPEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGIDIR	TQFIWMKYFSIFNTELSQSNIEERYKIQSY	
	GWKISIRGNRIWTLIDINGTKTSVFFPEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGIDIR	TQFIWMKYFSIFNTELSQSNIEERYKIQSY	
	GWKISIRGNRIWTLIDINGTKTSVFFPEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGIDIR	TQFIWMKYFSIFNTELSQSNIEERYKIQSY	
	GWKISIRGNRIWTLIDINGTKTSVFFPEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGIDIR	TQFIWMKYFSIFNTELSQSNIEERYKIQSY	
	*****	*****	*****	*****	
Original_Seq40	1081	1110 1111	1140 1141	1170 1171	1200
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPVGEILTRSKYNQNSKYINYRDLY	IGSEKPIIRRKSNQSINDDIVRKEDYIYLD	FFNLNQEHVYTYKIFKKEEKLFLAPISD	
	SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPVGEILTRSKYNQNSKYINYRDLY	IGSEKPIIRRKSNQSINDDIVRKEDYIYLD	FFNLNQEHVYTYKIFKKEEKLFLAPISD	
	SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPVGEILTRSKYNQNSKYINYRDLY	IGSEKPIIRRKSNQSINDDIVRKEDYIYLD	FFNLNQEHVYTYKIFKKEEKLFLAPISD	
	SEYLKDFWGNPLMYNKEYYMFNAGNKNSYI	KLKKDSPVGEILTRSKYNQNSKYINYRDLY	IGSEKPIIRRKSNQSINDDIVRKEDYIYLD	FFNLNQEHVYTYKIFKKEEKLFLAPISD	
	*****	*****	*****	*****	
Original_Seq40	1201	1230 1231	1260 1261	1290 1291	
Substitute_Seq40	-----	-----	-----	-----	-----
Amended_Seq40	-----	-----	-----	-----	-----
Whelan_M81186	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKRKPYNLKLGCNWFIPKDEGWT	E	
	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKRKPYNLKLGCNWFIPKDEGWT	E	
	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKRKPYNLKLGCNWFIPKDEGWT	E	
	SDEFYNTIQIKEYDEQPTYSCQLLFKKDEE	STDEIGLIGIHRFYESGIVFEEYKDYFCIS	KWYLKEVKRKPYNLKLGCNWFIPKDEGWT	E	
	*****	*****	*****	*****	

ALIGNMENT 5: SEQ ID NO:41

Original_Seq41	1	30 31	60 61	90 91	120
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	MQFVNKQPNFYKDPVNGVDIAYIKIPNVGQM	QPVKAFKIHKNWIPERDFTFNPEEGDLN	PPPEAKQVPVSYDYDSTYLSTDNEKDNLYLKG	VTKLPERIYSTDLGRMLLTSIVRGIPFWGG	
Original_Seq41	121	150 151	180 181	210 211	240
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	STIDTELKVIDTNCINVIQPDGYSRSEELN	LVIIGPSADI IQFECKSPGHEVLNLTNRNGY	GSTQYIRFSPDFTFGPEESLEVDTNPLLGA	GKPADTDPAVTLAHELHAGHRLYGIAINPN	
Original_Seq41	241	270 271	300 301	330 331	360
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	RVFKVNTNAYEYMSGLEVSFEELRTFGGHD	AKFIDSLQENEPRLYYNFKDIASTLNKA	KSI VGTASLQYMKNVPEKEYLLSEDTSGK	FSDVKLKFDPKLYKMLTEIYTDENFVKPFKV	
Original_Seq41	361	390 391	420 421	450 451	480
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	LNRKTYLNFDAVKFINIVPKVNYTIYDGF	NLRNTNLAANFNGQNTIINNMFNFKLNFT	GLFEYKLLCVRGIIITSKTKSLDKYGNKAL	NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE	NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
				NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE	NDLCIKVNNWDLFFSPSEDNFTNDLNKGEE
				*****	*****
Original_Seq41	481	510 511	540 541	570 571	600
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	ITSNTNIEAAEENISLDLIQQYYLTFNFDN	EPENISIEENLSSDIIGQLELMPNIEPFPNG	KKYELDKYTMFHYLRAQEFHKGSRIALTN	SVNEALLNPSRVYTFSSDYVKKVKNKATEA	SVNEALLNPSRVYTFSSDYVKKVKNKATEA
	ITSNTNIEAAEENISLDLIQQYYLTFNFDN	EPENISIEENLSSDIIGQLELMPNIEPFPNG	KKYELDKYTMFHYLRAQEFHKGSRIALTN	SVNEALLNPSRVYTFSSDYVKKVKNKATEA	SVNEALLNPSRVYTFSSDYVKKVKNKATEA
	ITSNTNIEAAEENISLDLIQQYYLTFNFDN	EPENISIEENLSSDIIGQLELMPNIEPFPNG	KKYELDKYTMFHYLRAQEFHKGSRIALTN	SVNEALLNPSRVYTFSSDYVKKVKNKATEA	SVNEALLNPSRVYTFSSDYVKKVKNKATEA
	*****	*****	*****	*****	*****
Original_Seq41	601	630 631	660 661	690 691	720
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	AMFLGWVEQLVYDFTDETSEVSTTDKIADI	TIIPYIGPALNIGMMLYKDDFVGALIFSG	AVILLEFIPEIAIPVLGTFALVSYIANKVL	TVQTDINALSKRNEKWDEVYKIVTNWLAK	TVQTDINALSKRNEKWDEVYKIVTNWLAK
	AMFLGWVEQLVYDFTDETSEVSTTDKIADI	TIIPYIGPALNIGMMLYKDDFVGALIFSG	AVILLEFIPEIAIPVLGTFALVSYIANKVL	TVQTDINALSKRNEKWDEVYKIVTNWLAK	TVQTDINALSKRNEKWDEVYKIVTNWLAK
	AMFLGWVEQLVYDFTDETSEVSTTDKIADI	TIIPYIGPALNIGMMLYKDDFVGALIFSG	AVILLEFIPEIAIPVLGTFALVSYIANKVL	TVQTDINALSKRNEKWDEVYKIVTNWLAK	TVQTDINALSKRNEKWDEVYKIVTNWLAK
	*****	*****	*****	*****	*****
Original_Seq41	721	750 751	780 781	810 811	840
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	VNTQIDILIRKKMKEALENQAATKAIINYO	YNOYTEEEKNNINFNIDDLSSKLNESINKA	MININKFLNQCSVSYLMNSMIPYGVKRLD	FDASLKDALIKYIDNNGTGLIGQVRLKDK	FDASLKDALIKYIDNNGTGLIGQVRLKDK
	VNTQIDILIRKKMKEALENQAATKAIINYO	YNOYTEEEKNNINFNIDDLSSKLNESINKA	MININKFLNQCSVSYLMNSMIPYGVKRLD	FDASLKDALIKYIDNNGTGLIGQVRLKDK	FDASLKDALIKYIDNNGTGLIGQVRLKDK
	VNTQIDILIRKKMKEALENQAATKAIINYO	YNOYTEEEKNNINFNIDDLSSKLNESINKA	MININKFLNQCSVSYLMNSMIPYGVKRLD	FDASLKDALIKYIDNNGTGLIGQVRLKDK	FDASLKDALIKYIDNNGTGLIGQVRLKDK
	*****	*****	*****	*****	*****
Original_Seq41	841	870 871	900 901	930 931	960
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	VNNTLSTDIPFQLSKYVDNQRLSTFTTEYI	KNIINTSILNLRYESNHLIDLSRYASKINI	GSKVNFDPIDKNQIQLFNLESSKIEVILKN	AIVVNSMYENFSTSFWRIPKYPFNSISLNN	AIVVNSMYENFSTSFWRIPKYPFNSISLNN
	VNNTLSTDIPFQLSKYVDNQRLSTFTTEYI	KNIINTSILNLRYESNHLIDLSRYASKINI	GSKVNFDPIDKNQIQLFNLESSKIEVILKN	AIVVNSMYENFSTSFWRIPKYPFNSISLNN	AIVVNSMYENFSTSFWRIPKYPFNSISLNN
	VNNTLSTDIPFQLSKYVDNQRLSTFTTEYI	KNIINTSILNLRYESNHLIDLSRYASKINI	GSKVNFDPIDKNQIQLFNLESSKIEVILKN	AIVVNSMYENFSTSFWRIPKYPFNSISLNN	AIVVNSMYENFSTSFWRIPKYPFNSISLNN
	*****	*****	*****	*****	*****
Original_Seq41	961	990 991	1020 1021	1050 1051	1080
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	EYTIINCMMENSGWKVSLNYGEI IWTLODT	QBIKQRVVFKYSQMINISDYINRWIFVTIT	NNRLNNSKIYINGRLIDQKPISNLGNLHA	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL
	EYTIINCMMENSGWKVSLNYGEI IWTLODT	QBIKQRVVFKYSQMINISDYINRWIFVTIT	NNRLNNSKIYINGRLIDQKPISNLGNLHA	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL
	EYTIINCMMENSGWKVSLNYGEI IWTLODT	QBIKQRVVFKYSQMINISDYINRWIFVTIT	NNRLNNSKIYINGRLIDQKPISNLGNLHA	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL	SNNIMFKLDGCRDTHRYIWKYFNLFDKEL
	*****	*****	*****	*****	*****
Original_Seq41	1081	1110 1111	1140 1141	1170 1171	1200
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	NEKEIKDLYDNQNSGILKDFWGDYLYQYDK	PYYMILLYDPNPKYVDVNNVGIRGYMYLKGP	RGSVMTTNIYLNSSLYRGTKPIIKKASGN	KDNIVRNNDRVYINVVVKNKEYRLATNASQ	KDNIVRNNDRVYINVVVKNKEYRLATNASQ
	NEKEIKDLYDNQNSGILKDFWGDYLYQYDK	PYYMILLYDPNPKYVDVNNVGIRGYMYLKGP	RGSVMTTNIYLNSSLYRGTKPIIKKASGN	KDNIVRNNDRVYINVVVKNKEYRLATNASQ	KDNIVRNNDRVYINVVVKNKEYRLATNASQ
	NEKEIKDLYDNQNSGILKDFWGDYLYQYDK	PYYMILLYDPNPKYVDVNNVGIRGYMYLKGP	RGSVMTTNIYLNSSLYRGTKPIIKKASGN	KDNIVRNNDRVYINVVVKNKEYRLATNASQ	KDNIVRNNDRVYINVVVKNKEYRLATNASQ
	*****	*****	*****	*****	*****
Original_Seq41	1201	1230 1231	1260 1261	1290 1297	
Substitute_Seq41	-----	-----	-----	-----	-----
Amended_Seq41	-----	-----	-----	-----	-----
Thompson_X52066	AGVEKILSALEIPDVGNLSQVVMKSKNDQ	GITNCKMNLQDNNGNDIGFIGFHQPNNIA	KLVASNWNYNQERSRSLGCSWEFIPVDD	GWGERPL	GWGERPL
	AGVEKILSALEIPDVGNLSQVVMKSKNDQ	GITNCKMNLQDNNGNDIGFIGFHQPNNIA	KLVASNWNYNQERSRSLGCSWEFIPVDD	GWGERPL	GWGERPL
	AGVEKILSALEIPDVGNLSQVVMKSKNDQ	GITNCKMNLQDNNGNDIGFIGFHQPNNIA	KLVASNWNYNQERSRSLGCSWEFIPVDD	GWGERPL	GWGERPL
	*****	*****	*****	*****	*****

ALIGNMENT 6: SEQ ID NO:42

Original_Seq42	1	30 31	60 61	90 91	120
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	MPVTINNPNYNDPIDNNNIIMMEPPFARGT	GRYYKAFKITDRIWIIPERYTFGYKPEDFN	KSSGIFNRDVCEYYDPDYLNTNDKKNIFLQ	TMIKLFNRIKSKPLGKLEMIINGIPYLG	
Original_Seq42	121	150 151	180 181	210 211	240
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	DRRVPLEEFNTNIASVTVNKLISNPGEVER	KKGIFANLIIFGPGVPLENENETIDIGIQNH	PASREGFGGIMQMKFCPEYVSFVNQVENK	GASIFNRRGYFSDPALILMHLEIHLHLGLY	
Original_Seq42	241	270 271	300 301	330 331	360
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	GIKVDDLPIVPNEKFFMQSDAIQAEELY	TFGGQDPSIITPSTDKSIYDKVLQNFGRIV	DRLNKVLVCISDPNININIKNFKDKYKF	VEDSEGKYSIDVESPDKLYKSLMFGFTETN	
Original_Seq42	361	390 391	420 421	450 451	480
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	IAENYKIKTRASYFSDSLPVKIKNLLDNE	IYTIIEEGFNISDKDMEYRGQNKAINKQA	YEEISKEHLAVYKIQMCKSVKAPGICIDVD	-----APGICIDVD NEDLFFIADKNSFDDLSKNERIEYNTQSN	-----APGICIDVD NEDLFFIADKNSFDDLSKNERIEYNTQSN
				-----APGICIDVD NEDLFFIADKNSFDDLSKNERIEYNTQSN	-----APGICIDVD NEDLFFIADKNSFDDLSKNERIEYNTQSN
				*****	*****
Original_Seq42	481	510 511	540 541	570 571	600
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	YIENDFPINELILDIDLISKIELPSENTES	LTDFNVDPVYVEKQPAIKKIPTDENTIFQY	LYSQTFFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGWVKQIVND	SFFSMDYIKTANKVVEAGLFAGWVKQIVND
	YIENDFPINELILDIDLISKIELPSENTES	LTDFNVDPVYVEKQPAIKKIPTDENTIFQY	LYSQTFFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGWVKQIVND	SFFSMDYIKTANKVVEAGLFAGWVKQIVND
	YIENDFPINELILDIDLISKIELPSENTES	LTDFNVDPVYVEKQPAIKKIPTDENTIFQY	LYSQTFFPLDIRDISLTSSFDDALLFSNKVY	SFFSMDYIKTANKVVEAGLFAGWVKQIVND	SFFSMDYIKTANKVVEAGLFAGWVKQIVND
	*****	*****	*****	*****	*****
Original_Seq42	601	630 631	660 661	690 691	720
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTTRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY
	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTTRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY
	FVIEANKSNTMDKIADISLIVPYIGLALNV	GNETAKGNFENAFIAGASILLEFIPELLI	PVVGAFLLSEYIDNKNKI IKTIDNALTTRN	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY	EKWSMDYGLIVAQWLSTVNTQFYTIKEGMY
	*****	*****	*****	*****	*****
Original_Seq42	721	750 751	780 781	810 811	840
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	KALNYQAQALEEIIKYRYNIYSEKEKSIN	IDFNDINSKLNEGINQAIDNINNPFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLNLYI	DENKLYLIGSAEYKSKVNKYLKTI MPFDL	DENKLYLIGSAEYKSKVNKYLKTI MPFDL
	KALNYQAQALEEIIKYRYNIYSEKEKSIN	IDFNDINSKLNEGINQAIDNINNPFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLNLYI	DENKLYLIGSAEYKSKVNKYLKTI MPFDL	DENKLYLIGSAEYKSKVNKYLKTI MPFDL
	KALNYQAQALEEIIKYRYNIYSEKEKSIN	IDFNDINSKLNEGINQAIDNINNPFINGCSV	SYLMKKMIPLAVEKLLDPDNTLKKNLNLYI	DENKLYLIGSAEYKSKVNKYLKTI MPFDL	DENKLYLIGSAEYKSKVNKYLKTI MPFDL
	*****	*****	*****	*****	*****
Original_Seq42	841	870 871	900 901	930 931	960
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	SIYTNDTILIEFMFNKYNSEILNIIILNLR	KDNNLIDLSGYAKVEYDGVDELNDKNQFK	LTSSANSKIRITQNONIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS
	SIYTNDTILIEFMFNKYNSEILNIIILNLR	KDNNLIDLSGYAKVEYDGVDELNDKNQFK	LTSSANSKIRITQNONIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS
	SIYTNDTILIEFMFNKYNSEILNIIILNLR	KDNNLIDLSGYAKVEYDGVDELNDKNQFK	LTSSANSKIRITQNONIIFNSVFLDFSVSF	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS	WIRIPKYKNDGIQNYIHNEYTIINCMMKNS
	*****	*****	*****	*****	*****
Original_Seq42	961	990 991	1020 1021	1050 1051	1080
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	GWKISIRGNRIIWTLIDINGKTKSVFPEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDI DR	TQFIWMKYFSIFNTELSQSNIERYKIQSY	TQFIWMKYFSIFNTELSQSNIERYKIQSY
	GWKISIRGNRIIWTLIDINGKTKSVFPEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDI DR	TQFIWMKYFSIFNTELSQSNIERYKIQSY	TQFIWMKYFSIFNTELSQSNIERYKIQSY
	GWKISIRGNRIIWTLIDINGKTKSVFPEYN	IREDISSEYINRWFFVTITNNLNNAKIYING	KLESNTDIKDIREVIANGEIIFKLDGDI DR	TQFIWMKYFSIFNTELSQSNIERYKIQSY	TQFIWMKYFSIFNTELSQSNIERYKIQSY
	*****	*****	*****	*****	*****
Original_Seq42	1081	1110 1111	1140 1141	1170 1171	1200
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	SEYLKDFWGNPLMYNKEYMFNAGNKNSY	IKLKKDSPVGEILTTSKYNQNSKYINRYDL	YIGKEKPIIRKKSNSQSINDDIVRKEDYIYL	DFPNLNQEWVRVYTYKPKKEEELFLAPIS	DFPNLNQEWVRVYTYKPKKEEELFLAPIS
	SEYLKDFWGNPLMYNKEYMFNAGNKNSY	IKLKKDSPVGEILTTSKYNQNSKYINRYDL	YIGKEKPIIRKKSNSQSINDDIVRKEDYIYL	DFPNLNQEWVRVYTYKPKKEEELFLAPIS	DFPNLNQEWVRVYTYKPKKEEELFLAPIS
	SEYLKDFWGNPLMYNKEYMFNAGNKNSY	IKLKKDSPVGEILTTSKYNQNSKYINRYDL	YIGKEKPIIRKKSNSQSINDDIVRKEDYIYL	DFPNLNQEWVRVYTYKPKKEEELFLAPIS	DFPNLNQEWVRVYTYKPKKEEELFLAPIS
	*****	*****	*****	*****	*****
Original_Seq42	1201	1230 1231	1260 1261	1290 1291	1292
Substitute_Seq42	-----	-----	-----	-----	-----
Amended_Seq42	-----	-----	-----	-----	-----
Whelan_M81186	DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE	ESTDEIGLIGIHRFPYESGIVFEEKDYFCI	SKWYLEVKKRPYNLKLGCNWQPIPKDEGW	TE	TE
	DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE	ESTDEIGLIGIHRFPYESGIVFEEKDYFCI	SKWYLEVKKRPYNLKLGCNWQPIPKDEGW	TE	TE
	DSDEFYNTIQIKEYDEQPTYSCQLLFKKDE	ESTDEIGLIGIHRFPYESGIVFEEKDYFCI	SKWYLEVKKRPYNLKLGCNWQPIPKDEGW	TE	TE
	*****	*****	*****	*****	*****